

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: BILLING-MEDEL, PATRICIA A.  
COHEN, MAURICE  
COLPITTS, TRACEY L.  
FRIEDMAN, PAULA N.  
HAYDEN, MARK  
KLASS, MICHAEL R.  
ROBERTS-RAPP, LISA  
RUSSELL, JOHN C.  
STROUPE, STEPHEN D.

(ii) TITLE OF THE INVENTION: REAGENTS AND METHODS FOR THE  
USEFUL FOR DETECTING DISEASES OF THE GASTROINTESTINAL  
TRACT

(iii) NUMBER OF SEQUENCES: 51

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Abbott Laboratories  
(B) STREET: 100 Abbott Park Road  
(C) CITY: Abbott Park  
(D) STATE: IL  
(E) COUNTRY: USA  
(F) ZIP: 60064-3500

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/828,856  
(B) FILING DATE: 31-MAR-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Becker, Cheryl L.  
(B) REGISTRATION NUMBER: 35,441  
(C) REFERENCE/DOCKET NUMBER: 6068.US.P1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 847/935-1729  
(B) TELEFAX: 847/938-2623  
(C) TELEX:

10025167 "121901

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCCAGGAATA	ACTAGAGAGG	AACAATGGGG	TTATTCAGAG	GTTTTGTTTT	CCTCTTAGTT	60
CTGTGCCTGC	TGCACCAAGTC	AAATACTTCC	TTCATTAAGC	TGAATAATAA	TGGCTTTGAA	120
GATATTGTCA	TTGTTATAGA	TCCTAGTGTG	CCAGAAGATG	AAAAAATAAT	TGAACAAATA	180
GAGGATATGG	TGACTACAGC	TTCTACGTAC	CTGTTTGAAG	CCACAGAAAA	AAGATTTTTT	240
T						241

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTAGAGAGGA	ACAATGGGGT	TATTCAGAGG	TTTTGTTTTT	CTCTTAGTTC	TGTGCCTGCT	60
GCACCAAGTCA	AATACTTCCT	TCATTAAGCT	GAATAATAAT	GGCTTTGAAG	ATATTGTCAT	120
TGTTATAGAT	CCTAGTGTGC	CAGAAGATGA	AAAAATAATT	GAACAAATAG	AGGATATGGT	180
GACTACAGCT	TCTACGTACC	TGTTTGAAGC	CACAGAAAA			219

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base\_polymorphism
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTNTGTAACG	AAAAAACCCA	TAATCAAGAA	GCTCCAAGCC	TACAAAACAT	AAAGTGCAAT	60
TTTAGAAGTA	CATGGGAGGT	GATTAGCAAT	TCTGAGGATT	TTAAAAACAC	CATACCCATG	120
GTGACACCAC	CTCCTCCACC	TGTCTTCTCA	TTGCTGAAGA	TCAGTCAAAG	AATTGTGTGC	180
TTAGTTCTTG	ATAAGTCTGG	AAGCATGGGG	GGTAAGGACC	GCCTAAATCG	A	231

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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TGGGGGGTAA	GGACCGCCTA	AATCGAATGA	ATCAAGCAGC	AAAACATTTC	CTGCTGCAGA	60
CTGTTGAAAA	TGGATCCTGG	GTGGGGGATGG	TTCACCTTTGA	TAGTACTGCC	ACTATTGTAA	120
ATAAGCTAAT	CCAAATAAAA	AGCAGTGATG	AAAGAAACAC	ACTCATGGCA	GGATTACCTA	180
CATATCCTCT	GGGAGGAACT	TCCATCTGCT	CTGGAATTAA	ATATGCATT	CAGGTGA	237

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTTCCATCTG	CTCTGGAATT	AAATATGCAT	TTCAGGTGAT	TGGAGAGCTA	CATTCCCAAC	60
TCGATGGATC	CGAAGTACTG	CTGCTGACTG	ATGGGGAGGA	TAACACTGCA	AGTTCTTGTA	120
TTGATGAAGT	GAAACAAAGT	GGGGCCATTG	TTCATTTTAT	TGCTTTGGGA	AGAGCTGCTG	180
ATGAAGCAGT	AATAGAGATG	AGCAAGATAA	CAGGAG			216

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base\_polymorphism
- (B) LOCATION: 24
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AATTGATAGT	ACAGTGGGAA	AGGNCACGTT	CTTTCTCATC	ACATGGAACA	GTCTGCCTCC	60
CAGTATTTCT	CTCTGGGATC	CCAGTGGAAC	AATAATGGAA	AATTTCACAG	TGGATGCAAC	120
TTCCAAAATG	GCCTATCTCA	GTATTCAGG	AAGTCAAAG	GTGGGCACTT	GGGCATACAA	180
TCTTCAAGCC	AAAGCGAACC	C				201

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCAAATTCTT	CTGTGCCTCC	AATCACAGTG	AATGCTAAAA	TGAATAAGGA	CGTAAACAGT	60
TTCCCCAGCC	CAATGATTGT	TTACGCAGAA	ATTCTACAAG	GATATGTACC	TGTTCTTGGA	120
GCCAATGTGA	CTGCTTTCAT	TGAATCACAG	AATGGACATA	CAGAAGTTTT	GGAACTTTTG	180
GATAATGGTG	CAGGCGCTGA	TTCTTTCAAG	AATGATGGAG	TCTACTCCAG	GTATTTTACA	240
G						241

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTGCAGGCGC	TGATTCTTTC	AAGAATGATG	GAGTCTACTC	CAGGTATTTT	ACAGCATATA	60
CAGAAAATGG	CAGATATAGC	TTAAAAGTTC	GGGCTCATGG	AGGAGCAAAC	ACTGCCAGGC	120
TAAAATTACG	GCCTCCACTG	AATAGAGCCG	CGTACATACC	AGGCTGGGTA	GTGAACGGGG	180
AAATTGAAGC	AAACCCGCCA	AGACCTGAAA	TTGATGAGGA	TACTCAGACC	ACCTTGGAGG	240
AT						242

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCCGCCAAGA	CCTGAAATTG	ATGAGGATAC	TCAGACCACC	TTGGAGGATT	TCAGCCGAAC	60
AGCATCCGGA	GGTGCAATTG	TGGTATCACA	AGTCCCAAGC	CTTCCCTTGC	CTGACCAATA	120
CCCACCAAGT	CAAATCACAG	ACCTTGATGC	CACAGTTCAT	GAGGATAAGA	TTATTCTTAC	180
ATGGACAGCA	CCAGGAGATA	ATTTTGATGT	TGGAAAAGTT	CAACGTTATA	TCA	233

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base\_polymorphism
- (B) LOCATION: 22
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(ix) FEATURE:

- (A) NAME/KEY: base\_polymorphism
- (B) LOCATION: 44
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCAATACCCA	CCAAGTCAAA	TNACAGACCT	TGATGCCACA	GTTNATGAGG	ATAAGATTAT	60
TCTTACATGG	ACAGCACCAG	GAGATAATTT	TGATGTTGGA	AAAGTTCAAC	GTTATATCAT	120
AAGAATAAGT	GCAAGTATTC	TTGATCTAAG	AGACAGTTTT	GATGATGCTC	TTCAAGTAAA	180
TACTACTGAT	CTGTCAACAA	AGGAGGCCAA	CTCCAAGGAA	AGCTTTGCAT	TTAAACCAGA	240
AAATATCTCA	GAAGAAAATG	CAACCCACAT	ATTTATTGCC	ATTAAAAGTA	TAGATAAAGC	300
ATTTGGCATC	AAA					313

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AAGTATTCTT	GATCTAAGAG	ACAGTTTTGA	TGATGCTCTT	CAAGTAAATA	CTACTGATCT	60
GTCACCAAAG	GAGGCCAACT	CCAAGGAAAG	CTTTGCATTT	AAACCAGAAA	ATATCTCAGA	120
AGAAAATGCA	ACCCACATAT	TTATTGCCAT	TAAAAGTATA	GATAAAAGCA	ATTTGACATC	180
AAAAGTATCC	AACATTGCAC	AAGTAACTTT	GTTTATCCCT	CAAGCAAATC	CTGATGACAT	240
TG						242

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base\_polymorphism
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(ix) FEATURE:

- (A) NAME/KEY: base\_polymorphism
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ANANAATGCA	ACCCACATAT	TTATTGCCAT	TAAAAGTATA	GATAAAAGCA	ATTTGACATC	60
AAAAGTATCC	AACATTGCAC	AAGTAACTTT	GTTTATCCCT	CAAGCAAATC	CTGATGACAT	120
TGATCCTACT	CCTACTCCTA	CTCCTACTCC	TGATAAAAGT	CATAATTCTG	GAGTTAATAT	180
TTCTACGCTG	GTATTGCTCTG	TGATTGGG				208

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTCCTACTCC	TACTCCTGAT	AAAAGTCATA	ATTCTGGAGT	TAATATTTCT	ACGCTGGTAT	60
TGTCTGTGAT	TGGGTCTGTT	GTAATTGTTA	ACTTTATTTT	AAGTACCACC	ATTTGAACCT	120
TAACGAAGAA	AAAAATCTTC	AAGTAGACCT	AGAAGAGAGT	TTTAAAAAAC	AAAACAATGT	180
AAGTAAAGGA	TATTTCTGAA	T				201

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base\_polymorphism
- (B) LOCATION: 111
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

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- (ix) FEATURE:  
 (A) NAME/KEY: base\_polymorphism  
 (B) LOCATION: 244  
 (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

- (ix) FEATURE:  
 (A) NAME/KEY: base\_polymorphism  
 (B) LOCATION: 284  
 (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TCTGTTGTAA	TTGTTAACTT	TATTTTAAAGT	ACCACCATT	GAACCTTAAC	GAAGAAAAAA	60
ATCTTCAAGT	AGACCTAGAA	GAGAGTTTTA	AAAAACAAAA	CAATGTAAGT	NAAGGATATT	120
TCTGAATCTT	AAAATTCATC	CCATGTGTGA	TCATAAACTC	ATAAAAAATA	TTTAAAGATG	180
TCGGAAAAGG	ATACTTTGAT	TAAATAAAAA	CACTCATGGA	TATGTAAAAA	CTGTCAAGAT	240
TAAATTTTAA	TAGTTTCATT	TATTTGTTAT	TTTATTTGTA	AGANATAGTG	ATGAACAAAG	300
A						301

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 229 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAAAAAAATC	TTCAAGTAGA	CCTAGAAGAG	AGTTTTTAAA	AACAAAACAA	TGTAAGTAAA	60
GGATATTTCT	GAATCTTAAA	ATTCATCCCA	TGTGTGATCA	TAAACTCATA	AAAATAATTT	120
TAAGATGTCT	GAAAAGGATA	CTTTGATTAA	ATAAAAACAC	TCATGGATAT	GTAAAAACTG	180
TCAAGATTAA	AATTTAATAG	TTTCATTTAT	TTGTTATTTT	ATTTGTAAG		229

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3043 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTAGAGAGGA	ACAATGGGGT	TATTCAGAGG	TTTTGTTTTT	CTCTTAGTTC	TGTGCCTGCT	60
GCACCAGTCA	AATACTTCCT	TCATTAAGCT	GAATAATAAT	GGCTTTGAAG	ATATTGTCAT	120
TGTTATAGAT	CCTAGTGTGC	CAGAAGATGA	AAAAATAATT	GAACAAATAG	AGGATATGGT	180
GACTACAGCT	TCTACGTACC	TGTTTGAAGC	CACAGAAAAA	AGATTTTTTT	TCAAAAATGT	240
ATCTATATTA	ATTCTGAGA	ATTGGAAGGA	AAATCCTCAG	TACAAAAGGC	CAAAACATGA	300
AAACCATAAA	CATGCTGATG	TTATAGTTGC	ACCACCTACA	CTCCCAGGTA	GAGATGAACC	360
ATACACCAAG	CAGTTCACAG	AATGTGGAGA	GAAAGGCGAA	TACATTCACT	TCACCCCTGA	420
CCTTCTACTT	GAAAAAAAAC	AAAATGAATA	TGGACCACCA	GGCAAACGTG	TTGTCCATGA	480
GTGGGCTCAC	CTCCGGTGGG	GAGTGTGTTG	TGAGTACAAT	GAAGATCAGC	CTTTCTACCG	540
TGCTAAGTCA	AAAAAAATCG	AAGCAACAAG	GTGTTCCGCA	GGTATCTCTG	GTAGAAATAG	600
AGTTTATAAG	TGTCAAGGAG	GCAGCTGTCT	TAGTAGAGCA	TGCAGAATTG	ATTCTACAAC	660
AAAACGTGAT	GGAAAAGATT	GTCAATTCTT	TCCTGATAAA	GTACAAACAG	AAAAAGCATC	720
CATAATGTTT	ATGCAAAGTA	TTGATTCTGT	TGTTGAATTT	TGTAACGAAA	AAACCCATAA	780
TCAAGAAGCT	CCAAGCCTAC	AAAACATAAA	GTGCAATTTT	AGAAGTACAT	GGGAGGTGAT	840
TAGCAATTCT	GAGGATTTTA	AAAACACCAT	ACCCATGGTG	ACACCACCTC	CTCCACCTGT	900

CTTCTCATTG	CTGAAGATCA	GTCAAAGAAT	TGTGTGCTTA	GTTCTTGATA	AGTCTGGAAG	960
CATGGGGGGT	AAGGACCGCC	TAAATCGAAT	GAATCAAGCA	GCAAAACATT	TCCTGCTGCA	1020
GACTGTTGAA	AATGGATCCT	GGGTGGGGAT	GGTTCACCTT	GATAGTACTG	CCACTATTGT	1080
AAATAAGCTA	ATCCAAATAA	AAAGCAGTGA	TGAAAGAAAC	ACACTCATGG	CAGGATTACC	1140
TACATATCCT	CTGGGAGGAA	CTTCCATCTG	CTCTGGAATT	AAATATGCAT	TTCAGGTGAT	1200
TGGAGAGCTA	CATTCCCAAC	TCGATGGATC	CGAAGTACTG	CTGCTGACTG	ATGGGGAGGA	1260
TAACACTGCA	AGTTCCTGTA	TTGATGAAGT	GAAACAAAGT	GGGGCCATTG	TTCATTTTAT	1320
TGCTTTGGGA	AGAGCTGCTG	ATGAAGCAGT	AATAGAGATG	AGCAAGATAA	CAGGAGGAAG	1380
TCATTTTTAT	GTTTCAGATG	AAGCTCAGAA	CAATGGCCTC	ATTGATGCTT	TTGGGGCTCT	1440
TACATCAGGA	AATACTGATC	TCTCCAGAA	GTCCCTTCAG	CTCGAAAGTA	AGGGATTAAAC	1500
ACTGAATAGT	AATGCCTGGA	TGAACGACAC	TGTCATAATT	GATAGTACAG	TGGGAAAGGA	1560
CACGTTCTTT	CTCATCACAT	GGAACAGTCT	GCCTCCAGT	ATTTCTCTCT	GGGATCCCG	1620
TGGAACAATA	ATGGAAAATT	TCACAGTGGG	TGCAACTTCC	AAAATGGCCT	ATCTCAGTAT	1680
TCCAGGAAC	GCAAAGGTGG	GCACTTGGGC	ATACAATCTT	CAAGCCAAAG	CGAACCCAGA	1740
AACATTAAC	ATTACAGTAA	CTTCTCGAGC	AGCAAAATCT	TCTGTGCCTC	CAATCACAGT	1800
GAATGCTAAA	ATGAATAAGG	ACGTAAACAG	TTTCCCCAGC	CCAATGATTG	TTTACGCAGA	1860
AATTTCTACA	GGATATGTAC	CTGTTCTTGG	AGCCAATGTG	ACTGCTTTCA	TTGAATCACA	1920
GAATGGACAT	ACAGAAGTTT	TGGAACTTTT	GGATAATGGT	GCAGGCGCTG	ATTCTTTCAA	1980
GAATGATGGA	GTCTACTCCA	GGTATTTTAC	AGCATATACA	GAAAATGGCA	GATATAGCTT	2040
AAAAGTTCGG	GCTCATGGAG	GAGCAAACAC	TGCCAGGCTA	AAATTACGGC	CTCCACTGAA	2100
TAGAGCCGCG	TACATACCAG	GCTGGGTAGT	GAACGGGGAA	ATTGAAGCAA	ACCCGCCAAG	2160
ACCTGAAATT	GATGAGGATA	CTCAGACCAC	CTTGGAGGAT	TTGAGCCGAA	CAGCATCCGG	2220
AGGTGCATTT	GTGGTATCAC	AAGTCCCAAG	CCTTCCCTTG	CCTGACCAAT	ACCCACCAAG	2280
TCAAATCACA	GACCTTGATG	CCACAGTTCA	TGAGGATAAG	ATTATTCTTA	CATGGACAGC	2340
ACCAGGAGAT	AATTTTGATG	TTGGAAAAGT	TCAACGTTAT	ATCATAAGAA	TAAGTGCAAG	2400
TATTCTTGAT	CTAAGAGACA	GTTTTGATGA	TGCTCTTCAA	GTAAATACTA	CTGATCTGTC	2460
ACCAAAGGAG	GCCAACTCCA	AGGAAAGCTT	TGCATTTAAA	CCAGAAAATA	TCTCAGAAGA	2520
AAATGCAACC	CACATATTTA	TTGCCATTAA	AAGTATAGAT	AAAAGCAATT	TGACATCAAA	2580
AGTATCCAAC	ATTGCACAAG	TAACTTTGTT	TATCCCTCAA	GCAAATCCTG	ATGACATTGA	2640
TCCTACTCCT	ACTCTACTCT	CTACTCCTGA	TAAAAGTCAT	AATTCTGGAG	TTAATATTTT	2700
TACGCTGGTA	TTGTCTGTGA	TTGGGTCTGT	TGTAATTGTT	AACTTTATTT	TAAGTACCAC	2760
CATTTGAACC	TTAACGAAGA	AAAAAATCTT	CAAGTAGACC	TAGAAGAGAG	TTTTAAAAAA	2820
CAAAACAATG	TAAGTAAAGG	ATATTTCTGA	ATCTTAAAAA	TCATCCCATG	TGTGATCATA	2880
AACTCATAAA	AATAATTTTA	AGATGTCGGA	AAAGGATACT	TTGATTAAAT	AAAAACACTC	2940
ATGGATATGT	AAAAACTGTC	AAGATTAAAA	TTTAATAGTT	TCATTTATTT	GTTATTTTAT	3000
TTGTAAGAAA	TAGTGATGAA	CAAAGATCCT	TTTTCATACT	GAT		3043

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1399 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCAAAATCTT	CTGTGCCTCC	AATCACAGTG	AATGCTAAAA	TGAATAAGGA	CGTAAACAGT	60
TTCCCCAGCC	CAATGATTGT	TTACGCAGAA	ATTCTACAAG	GATATGTACC	TGTTCTTGGA	120
GCCAAATGTA	CTGCTTTCAT	TGAATCACAG	AATGGACATA	CAGAAGTTTT	GGAACTTTTG	180
GATAATGGTG	CAGGCGCTGA	TTCTTTCAAG	AATGATGGAG	TCTACTCCAG	GTATTTTACA	240
GCATATACAG	AAAATGGCAG	ATATAGCTTA	AAAGTTCGGG	CTCATGGAGG	AGCAAACACT	300
GCCAGGCTAA	AATTACGGCC	TCCACTGAAT	AGAGCCGCGT	ACATACCAGG	CTGGGTAGTG	360
AACGGGGAAA	TTGAAGCAAA	CCCGCCAAGA	CCTGAAATTG	ATGAGGATAC	TCAGACCACC	420
TTGGAGGATT	TCAGCCGAAC	AGCATCCGGA	GGTGCAATTG	TGGTATCACA	AGTCCCAAGC	480
CTTCCCTTGC	CTGACCAATA	CCCACCAAGT	CAAAATCACAG	ACCTTGATGC	CACAGTTCAT	540
GAGGATAAGA	TTATTCTTAC	ATGGACAGCA	CCAGGAGATA	ATTTTGATGT	TGGAAAAGTT	600
CAACGTTTATA	TCATAAGAAT	AAGTGCAAGT	ATTCTTGATC	TAAGAGACAG	TTTTTGATGAT	660
GCTCTTCAAG	TAAATACTAC	TGATCTGTCA	CCAAAGGAGG	CCAACTCCAA	GGAAAGCTTT	720
GCATTTAAAC	CAGAAAATAT	CTCAGAAGAA	AATGCAACCC	ACATATTTAT	TGCCATATAA	780
AGTATAGATA	AAAGCAATTT	GACATCAAAA	GTATCCAAAC	TTGCACAAGT	AACCTTGTTT	840
ATCCCTCAAG	CAAATCCTGA	TGACATTGAT	CCTACTCCTA	CTCCTACTCC	TACTCCTGAT	900
AAAAGTCATA	ATTCTGGAGT	TAATATTTCT	ACGCTGGTAT	TGTCTGTGAT	TGGGTCTGTT	960
GTAATTGTTA	ACTTTATTTT	AAGTACCACC	ATTTGAACCT	TAACGAAGAA	AAAAATCTTC	1020

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AAGTAGACCT	AGAAGAGAGT	TTTAAAAAAC	AAAACAATGT	AAGTAAAGGA	TATTTCTGAA	1080
TCCTTAAAAAT	CATCCCATGT	GTGATCATAA	ACTCATAAAA	ATAATTTTAA	GATGTCGGGA	1140
AAGGATACTT	TGATTAAATA	AAAACACTCA	TGGATATGTA	AAAACCTGTA	AGATTAAAAAT	1200
TTAATAGTTT	CATTTATTTG	TTATTTTATT	TGTAAGAAAT	AGTGATGAAC	AAAGATCCTT	1260
TTTCATACTG	ATACCTGGTT	GTATATTATT	TGATGCAACA	GTTTTCTGAA	ATGATATTTC	1320
AAATTGCATC	AAGAAATTAA	AATCATCTAT	CTGAGTAGTC	AAAATACAAG	TAAAGGAGAG	1380
CAAATAAACA	ACATTTGGA					1399

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3181 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GCCAGGAATA	ACTAGAGAGG	AACAATGGGG	TTATTCAGAG	GTTTTGTTTT	CCTCTTAGTT	60
CTGTGCCTGC	TGCACCAGTC	AAATACTTCC	TTCATTAAGC	TGAATAATAA	TGGCTTTGAA	120
GATATTGTCA	TTGTTATAGA	TCCTAGTGTG	CCAGAAGATG	AAAAAATAAT	TGAACAAATA	180
GAGGATATGG	TGACTACAGC	TTCTACGTAC	CTGTTTGAAG	CCACAGAAAA	AAGATTTTTT	240
TTCAAAAAATG	TATCTATATT	AATTCCTGAG	AATTGGAAGG	AAAATCCTCA	GTACAAAAGG	300
CCAAAACATG	AAAACCATAA	ACATGCTGAT	GTTATAGTTG	CACCACCTAC	ACTCCCAGGT	360
AGAGATGAAC	CATACACCAA	GCAGTTCACA	GAATGTGGAG	AGAAAGGCGA	ATACATTTCAC	420
TTCAACCCCTG	ACCTTCTACT	TGAAAAAATA	CAAAATGAAT	ATGGACCACC	AGGCAAACTG	480
TTTGTCCTAG	AGTGGGCTCA	CCTCCGGTGG	GGAGTGTGTT	ATGAGTACAA	TGAAGATCAG	540
CCTTTCTACC	GTGCTAAGTC	AAAAAAAATC	GAAGCAACAA	GGTGTTCGCG	AGGTATCTCT	600
GGTAGAAATA	GAGTTTATAA	GTGTCAAGGA	GGCAGCTGTC	TTAGTAGAGC	ATGCAGAATT	660
GATTCACAA	CAAAACTGTA	TGGAAAAGAT	TGTCAATTCT	TTCTTGATAA	AGTACAAACA	720
GAAAAAGCAT	CCATAATGTT	TATGCAAAAGT	ATTGATTCTG	TTGTTGAATT	TTGTAACGAA	780
AAAACCCATA	ATCAAGAAGC	TCCAAGCCTA	CAAAACATAA	AGTGCAATTT	TAGAAGTACA	840
TGGGAGGTGA	TTAGCAATTC	TGAGGATTTT	AAAAACACCA	TACCCATGGT	GACACCACCT	900
CCTCCACCTG	TCTTCTCATT	GCTGAAGATC	AGTCAAAGAA	TTGTGTGCTT	AGTTCTTGAT	960
AAGTCTGGAA	GCATGGGGGG	TAAGGACCGC	CTAAATCGAA	TGAATCAAGC	AGCAAAACAT	1020
TTCTGTGTC	AGACTGTTGA	AAATGGATCC	TGGGTGGGGA	TGGTTCACTT	TGATAGTACT	1080
GCCACTATTG	TAAATAAGCT	AATCCAAATA	AAAAGCAGTG	ATGAAAGAAA	CACACTCATG	1140
GCAGGATTAC	CTACATATCC	TCTGGGAGGA	ACTTCCATCT	GCTCTGGAAT	TAAATATGCA	1200
TTTCAGGTGA	TTGGAGAGCT	ACATTCCCAA	CTCGATGGAT	CCGAAGTACT	GCTGCTGACT	1260
GATGGGGAGG	ATAACACTGC	AAGTTCTTGT	ATTGATGAAG	TGAAACAAAG	TGGGGCCATT	1320
GTTCAATTTA	TTGCTTTGGG	AAGAGCTGCT	GATGAAGCAG	TAATAGAGAT	GAGCAAGATA	1380
ACAGGAGGAA	GTCATTTTTA	TGTTTCAGAT	GAAGCTCAGA	ACAATGGCCT	CATTGATGCT	1440
TTTGGGGGCT	TTACATCAGG	AAATACTGAT	CTCTCCCGAG	AGTCCCTTCA	GCTCGAAAGT	1500
AAGGGATTAA	CACGTAATAG	TAATGCCTGG	ATGAACGACA	CTGTACATAA	TGATAGTACA	1560
GTGGGAAAGG	ACACGTTCTT	TCTCATCACA	TGGAACAGTC	TGCCTCCCG	TATTTCTCTC	1620
TGGGATCCCA	GTGGAACAAT	AATGGAAAAT	TTACAGTGGG	ATGCAACTTC	CAAAATGGCC	1680
TATCTCAGTA	TTCCAGGAAC	TGCAAGGCTG	GGCACTTGGG	CATACAATCT	TCAAGCCAAA	1740
GCGAACCCAG	AAACATTAAC	TATTACAGTA	ACTTCTCGAG	CAGCAAATTC	TTCTGTGCTT	1800
CCAATCACAG	TGAATGCTAA	AATGAATAAG	GACGTAAACA	GTTTCCCGAG	CCCAATGATT	1860
GTTTACGCAG	AAATTCTACA	AGGATATGTA	CCTGTTCTTG	GAGCCAATGT	GACTGCTTTC	1920
ATTGAATCAC	AGAATGGACA	TACAGAAGTT	TTGGAACCTT	TGGATAATGG	TGCAGGCGCT	1980
GATTCTTTCA	AGAATGATGG	AGTCTACTCC	AGGTATTTTA	CAGCATATAC	AGAAAATGGC	2040
AGATATAGCT	TAAAAGTTCT	GGCTCATGGA	GGAGCAAACA	CTGCCAGGCT	AAAATTACGG	2100
CCTCCACTGA	ATAGAGCCGC	GTACATACCA	GGCTGGGTAG	TGAACGGGGA	AATTGAAGCA	2160
AACCCGCCAA	GACCTGAAAT	TGATGAGGAT	ACTCAGACCA	CCTTGGAGGA	TTTCAGCCGA	2220
ACAGCATCCG	GAGGTGCATT	TGTGGTATCA	CAAGTCCCAA	GCCTTCCCTT	GCCTGACCAA	2280
TACCCACCAA	GTCAAATCAC	AGACCTTGAT	GCCACAGTTC	ATGAGGATAA	GATTATTCTT	2340
ACATGGACAG	CACCAAGAGA	TAATTTTGAT	GGTGGAAAAG	TTCAACGTTA	TATCATAAGA	2400
ATAAGTGCAA	GTATTCTTGA	TCTAAGAGAC	AGTTTTGATG	ATGCTCTTCA	AGTAAATACT	2460
ACTGATCTGT	CACCAAAGGA	GGCCAACTCC	AAGGAAAGCT	TTGCATTTAA	ACCAGAAAAT	2520
ATCTCAGAAG	AAAATGCAAC	CCACATATTT	ATTGCCATTA	AAAGTATAGA	TAAAGCAAT	2580
TTGACATCAA	AAGTATCCAA	CATTGCACAA	GCTACTTTGT	TTATCCCTCA	AGCAAATCCT	2640
GATGACATTG	ATCCTACTCC	TACTCTACTC	CTACTCCTG	ATAAAAGTCA	TAATTTCTGA	2700
GTTAATATTT	CTACGCTGGT	ATTGTCTGTG	ATTGGGTCTG	TTGTAATTGT	TAACCTTTATT	2760
TTAAGTACCA	CCATTTGAAC	CTTAACGAAG	AAAAAAATCT	TCAAGTAGAC	CTAGAAGAGA	2820



GTTTTAAAAA	ACAAAACAAT	GTAAGTAAAG	GATATTTCTG	AATCTTAAAA	TTCATCCCAT	2880
GTGTGATCAT	AAACTCATAA	AAATAATTTT	AAGATGTCGG	AAAAGGATAC	TTTGATTAAA	2940
TAAAAACACT	CATGGATATG	TAAAAACTGT	CAAGATTAAA	ATTTAATAGT	TTCATTTATT	3000
TGTTATTTTA	TTTGTAAGAA	ATAGTGATGA	ACAAAGATCC	TTTTTCATAC	TGATACCTGG	3060
TTGTATATTA	TTTGATGCAA	CAGTTTCTG	AAATGATATT	TCAAATTGCA	TCAAGAAATT	3120
AAAATCATCT	ATCTGAGTAG	TCAAAATACA	AGTAAAGGAG	AGCAAATAAA	CAACATTTGG	3180
A						3181

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGCTCGGAAT	TCCGAGCTTG	GATCCTCTAG	AGCGGCCGCC	GACTAGTGAG	CTCGTCGACC	60
CGGGAATT						68

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AATTAATTCC	CGGGTCGACG	AGCTCACTAG	TCGGCGGCCG	CTCTAGAGGA	TCCAAGCTCG	60
GAATTCCG						68

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AGCGGATAAC	AATTTACAC	AGGA	24
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(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TGTAAAACGA	CGGCCAGT	18
------------	----------	----

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs

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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CTGCCAGGCT AAAATTACGG

20

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATCACAGACC TTGATGCCAC

20

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCTGGTATTG TCTGTGATTG GGTC

24

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CATCAGGATT TGCTTGAGGG

20

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TATTGGTCAG GCAAGGGAAG

20

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTGTTTGCTC CTCCATGAGC

20

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAAGTAGAAG GTCAGGGGTG

20

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATAAGTGTCA AGGAGGCAGC

20

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCAGACTGTT CCATGTGATG

20

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATGTACCTGT TCTTGAGGCC

20

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ACGTACCTGT TTGAAGCCAC

20

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGTAAGGACC GCCTAAATCG

20

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GAAGTGAAAC AAAGTGGGGC

20

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TTATCCTCCC CATCAGTCAG

20

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TCGATTTAGG CGGTCCTTAC

20

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TGTGGCTTCA AACAGGTACG

20

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GGGTAAGGAC CGCCTAAATC GAATG

25

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GAGCCCCAAA AGCATCAATG AGG

23

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 917 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Met	Gly	Leu	Phe	Arg	Gly	Phe	Val	Phe	Leu	Leu	Val	Leu	Cys	Leu	Leu
1				5					10					15	
His	Gln	Ser	Asn	Thr	Ser	Phe	Ile	Lys	Leu	Asn	Asn	Asn	Gly	Phe	Glu
			20					25					30		
Asp	Ile	Val	Ile	Val	Ile	Asp	Pro	Ser	Val	Pro	Glu	Asp	Glu	Lys	Ile
		35					40					45			
Ile	Glu	Gln	Ile	Glu	Asp	Met	Val	Thr	Thr	Ala	Ser	Thr	Tyr	Leu	Phe
	50					55				60					
Glu	Ala	Thr	Glu	Lys	Arg	Phe	Phe	Phe	Lys	Asn	Val	Ser	Ile	Leu	Ile
65					70					75				80	
Pro	Glu	Asn	Trp	Lys	Glu	Asn	Pro	Gln	Tyr	Lys	Arg	Pro	Lys	His	Glu
			85						90					95	
Asn	His	Lys	His	Ala	Asp	Val	Ile	Val	Ala	Pro	Pro	Thr	Leu	Pro	Gly
			100					105					110		
Arg	Asp	Glu	Pro	Tyr	Thr	Lys	Gln	Phe	Thr	Glu	Cys	Gly	Glu	Lys	Gly
		115					120					125			
Glu	Tyr	Ile	His	Phe	Thr	Pro	Asp	Leu	Leu	Leu	Glu	Lys	Lys	Gln	Asn
	130						135				140				
Glu	Tyr	Gly	Pro	Pro	Gly	Lys	Leu	Phe	Val	His	Glu	Trp	Ala	His	Leu
145					150					155					160

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Arg	Trp	Gly	Val	Phe	Asp	Glu	Tyr	Asn	Glu	Asp	Gln	Pro	Phe	Tyr	Arg	
				165					170					175		
Ala	Lys	Ser	Lys	Lys	Ile	Glu	Ala	Thr	Arg	Cys	Ser	Ala	Gly	Ile	Ser	
			180					185					190			
Gly	Arg	Asn	Arg	Val	Tyr	Lys	Cys	Gln	Gly	Gly	Ser	Cys	Leu	Ser	Arg	
		195					200					205				
Ala	Cys	Arg	Ile	Asp	Ser	Thr	Thr	Lys	Leu	Tyr	Gly	Lys	Asp	Cys	Gln	
	210					215					220					
Phe	Phe	Pro	Asp	Lys	Val	Gln	Thr	Glu	Lys	Ala	Ser	Ile	Met	Phe	Met	
225					230					235					240	
Gln	Ser	Ile	Asp	Ser	Val	Val	Glu	Phe	Cys	Asn	Glu	Lys	Thr	His	Asn	
				245					250					255		
Gln	Glu	Ala	Pro	Ser	Leu	Gln	Asn	Ile	Lys	Cys	Asn	Phe	Arg	Ser	Thr	
			260					265					270			
Trp	Glu	Val	Ile	Ser	Asn	Ser	Glu	Asp	Phe	Lys	Asn	Thr	Ile	Pro	Met	
		275					280					285				
Val	Thr	Pro	Pro	Pro	Pro	Pro	Val	Phe	Ser	Leu	Leu	Lys	Ile	Ser	Gln	
	290					295					300					
Arg	Ile	Val	Cys	Leu	Val	Leu	Asp	Lys	Ser	Gly	Ser	Met	Gly	Gly	Lys	
305					310					315					320	
Asp	Arg	Leu	Asn	Arg	Met	Asn	Gln	Ala	Ala	Lys	His	Phe	Leu	Leu	Gln	
				325					330					335		
Thr	Val	Glu	Asn	Gly	Ser	Trp	Val	Gly	Met	Val	His	Phe	Asp	Ser	Thr	
			340					345					350			
Ala	Thr	Ile	Val	Asn	Lys	Leu	Ile	Gln	Ile	Lys	Ser	Ser	Asp	Glu	Arg	
		355					360					365				
Asn	Thr	Leu	Met	Ala	Gly	Leu	Pro	Thr	Tyr	Pro	Leu	Gly	Gly	Thr	Ser	
	370					375					380					
Ile	Cys	Ser	Gly	Ile	Lys	Tyr	Ala	Phe	Gln	Val	Ile	Gly	Glu	Leu	His	
385					390					395					400	
Ser	Gln	Leu	Asp	Gly	Ser	Glu	Val	Leu	Leu	Thr	Asp	Gly	Glu	Asp		
			405					410					415			
Asn	Thr	Ala	Ser	Ser	Cys	Ile	Asp	Glu	Val	Lys	Gln	Ser	Gly	Ala	Ile	
			420					425					430			
Val	His	Phe	Ile	Ala	Leu	Gly	Arg	Ala	Ala	Asp	Glu	Ala	Val	Ile	Glu	
		435					440					445				
Met	Ser	Lys	Ile	Thr	Gly	Gly	Ser	His	Phe	Tyr	Val	Ser	Asp	Glu	Ala	
	450					455					460					
Gln	Asn	Asn	Gly	Leu	Ile	Asp	Ala	Phe	Gly	Ala	Leu	Thr	Ser	Gly	Asn	
465					470					475					480	
Thr	Asp	Leu	Ser	Gln	Lys	Ser	Leu	Gln	Leu	Glu	Ser	Lys	Gly	Leu	Thr	
				485					490					495		
Leu	Asn	Ser	Asn	Ala	Trp	Met	Asn	Asp	Thr	Val	Ile	Ile	Asp	Ser	Thr	
			500					505					510			
Val	Gly	Lys	Asp	Thr	Phe	Phe	Leu	Ile	Thr	Trp	Asn	Ser	Leu	Pro	Pro	
		515					520					525				
Ser	Ile	Ser	Leu	Trp	Asp	Pro	Ser	Gly	Thr	Ile	Met	Glu	Asn	Phe	Thr	
	530					535					540					
Val	Asp	Ala	Thr	Ser	Lys	Met	Ala	Tyr	Leu	Ser	Ile	Pro	Gly	Thr	Ala	
545					550					555					560	
Lys	Val	Gly	Thr	Trp	Ala	Tyr	Asn	Leu	Gln	Ala	Lys	Ala	Asn	Pro	Glu	
				565					570					575		
Thr	Leu	Thr	Ile	Thr	Val	Thr	Ser	Arg	Ala	Ala	Asn	Ser	Ser	Val	Pro	
			580					585					590			
Pro	Ile	Thr	Val	Asn	Ala	Lys	Met	Asn	Lys	Asp	Val	Asn	Ser	Phe	Pro	
		595					600					605				
Ser	Pro	Met	Ile	Val	Tyr	Ala	Glu	Ile	Leu	Gln	Gly	Tyr	Val	Pro	Val	
	610					615					620					
Leu	Gly	Ala	Asn	Val	Thr	Ala	Phe	Ile	Glu	Ser	Gln	Asn	Gly	His	Thr	
625					630					635					640	
Glu	Val	Leu	Glu	Leu	Leu	Asp	Asn	Gly	Ala	Gly	Ala	Asp	Ser	Phe	Lys	
				645					650					655		
Asn	Asp	Gly	Val	Tyr	Ser	Arg	Tyr	Phe	Thr	Ala	Tyr	Thr	Glu	Asn	Gly	
			660					665					670			
Arg	Tyr	Ser	Leu	Lys	Val	Arg	Ala	His	Gly	Gly	Ala	Asn	Thr	Ala	Arg	
		675					680						685			

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Leu Lys Leu Arg Pro Pro Leu Asn Arg Ala Ala Tyr Ile Pro Gly Trp  
690 695 700  
Val Val Asn Gly Glu Ile Glu Ala Asn Pro Pro Arg Pro Glu Ile Asp  
705 710 715 720  
Glu Asp Thr Gln Thr Thr Leu Glu Asp Phe Ser Arg Thr Ala Ser Gly  
725 730 735  
Gly Ala Phe Val Val Ser Gln Val Pro Ser Leu Pro Leu Pro Asp Gln  
740 745 750  
Tyr Pro Pro Ser Gln Ile Thr Asp Leu Asp Ala Thr Val His Glu Asp  
755 760 765  
Lys Ile Ile Leu Thr Trp Thr Ala Pro Gly Asp Asn Phe Asp Val Gly  
770 775 780  
Lys Val Gln Arg Tyr Ile Ile Arg Ile Ser Ala Ser Ile Leu Asp Leu  
785 790 795 800  
Arg Asp Ser Phe Asp Asp Ala Leu Gln Val Asn Thr Thr Asp Leu Ser  
805 810 815  
Pro Lys Glu Ala Asn Ser Lys Glu Ser Phe Ala Phe Lys Pro Glu Asn  
820 825 830  
Ile Ser Glu Glu Asn Ala Thr His Ile Phe Ile Ala Ile Lys Ser Ile  
835 840 845  
Asp Lys Ser Asn Leu Thr Ser Lys Val Ser Asn Ile Ala Gln Val Thr  
850 855 860  
Leu Phe Ile Pro Gln Ala Asn Pro Asp Asp Ile Asp Pro Thr Pro Thr  
865 870 875 880  
Pro Thr Pro Thr Pro Asp Lys Ser His Asn Ser Gly Val Asn Ile Ser  
885 890 895  
Thr Leu Val Leu Ser Val Ile Gly Ser Val Val Ile Val Asn Phe Ile  
900 905 910  
Leu Ser Thr Thr Ile  
915

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Ala Asn Ser Ser Val Pro Pro Ile Thr Val Asn Ala Lys Met Asn Lys  
1 5 10 15  
Asp Val Asn Ser Phe  
20

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Asp Asn Gly Ala Gly Ala Asp Ser Phe Lys Asn Asp Gly Val Tyr Ser  
1 5 10 15  
Arg Tyr Phe Thr Ala Tyr Thr Glu Asn Gly Arg Tyr Ser Leu Lys  
20 25 30

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Val	Arg	Ala	His	Gly	Gly	Ala	Asn	Thr	Ala	Arg	Leu	Lys	Leu	Arg	Pro
1				5					10				15		
Pro	Leu	Asn	Arg	Ala	Ala	Tyr	Ile								
				20											

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Ser	Leu	Pro	Leu	Pro	Asp	Gln	Tyr	Pro	Pro	Ser	Gln	Ile	Thr	Asp	Leu
1				5					10					15	
Asp	Ala	Thr	Val	His	Glu	Asp	Lys	Ile	Ile	Leu	Thr	Trp	Thr	Ala	Pro
			20					25					30		
Gly	Asp	Asn	Phe	Asp	Val	Gly	Lys								
		35					40								

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Tyr	Asn	Glu	Asp	Gln	Pro	Phe	Tyr	Arg	Ala	Lys	Ser	Lys	Lys	Ile	Glu
1				5					10					15	
Ala	Thr	Arg	Cys												
			20												

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:



Leu Ser Arg Ala Cys Arg Ile Asp Ser Thr Thr Lys Leu Tyr Gly Lys  
 1 5 10 15  
 Asp Cys Gln Phe Phe Pro Asp Lys  
 20

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Lys Ser Ser Asp Glu Arg Asn Thr Leu Met Ala Gly Leu Pro Thr Tyr  
 1 5 10 15  
 Pro Leu Gly Gly  
 20

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Glu Ile Asp Glu Asp Thr Gln Thr Thr Leu Glu Asp Phe Ser Arg  
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 8 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Asp Tyr Lys Asp Asp Asp Asp Lys  
 1 5

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

10065167 161901

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Met His Thr Glu His  
1 5 10 15  
His His His His His  
20